

Fig. 1

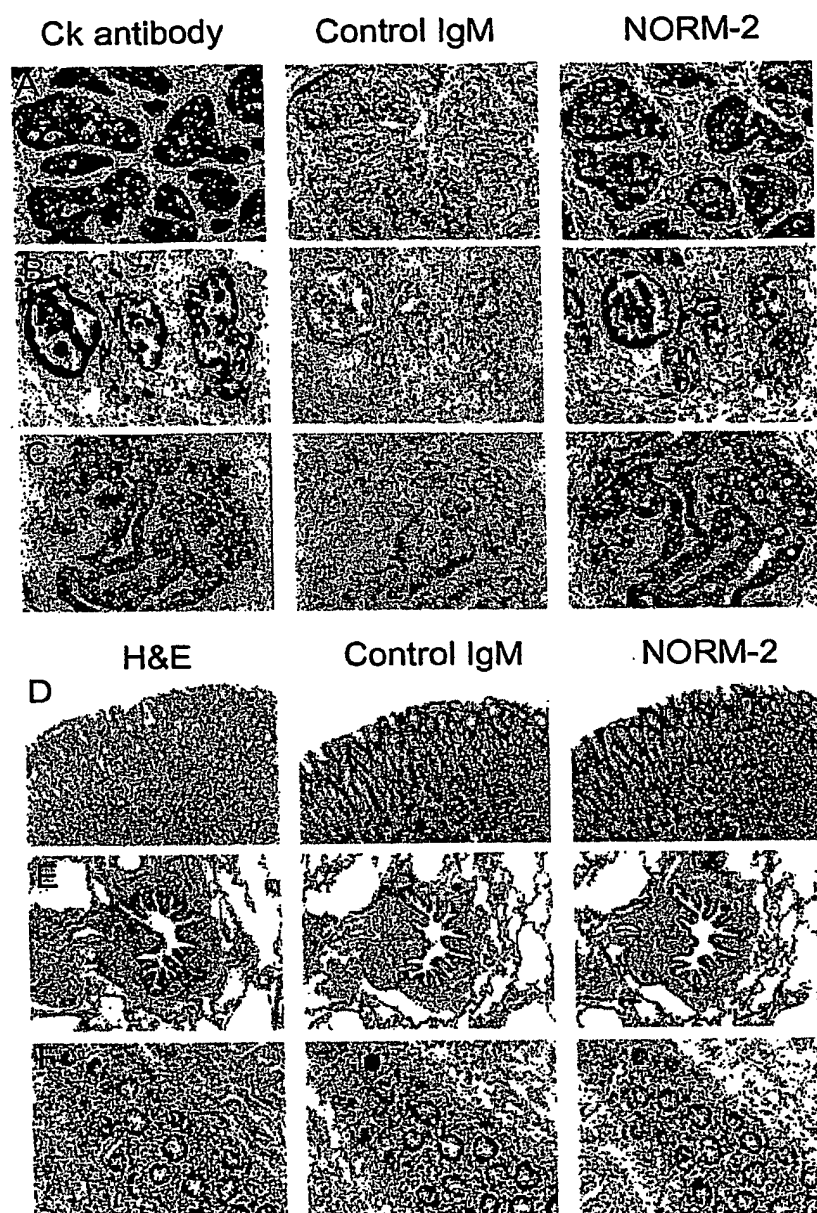


Fig. 2

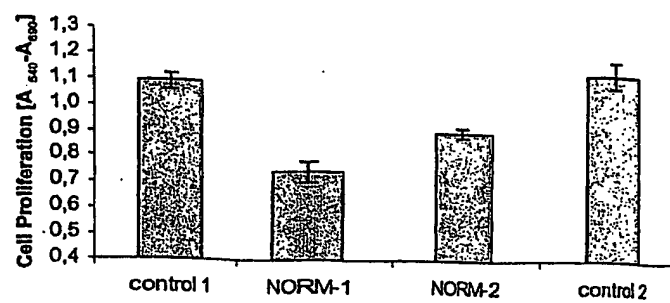


Fig. 3

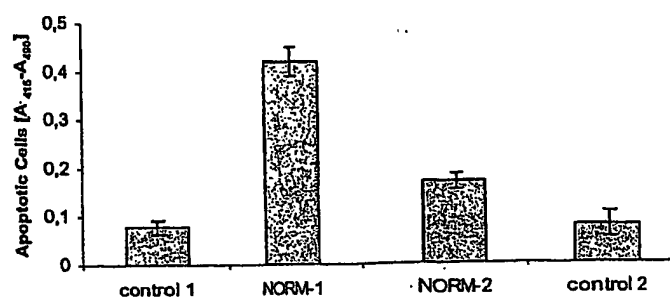


Fig. 4

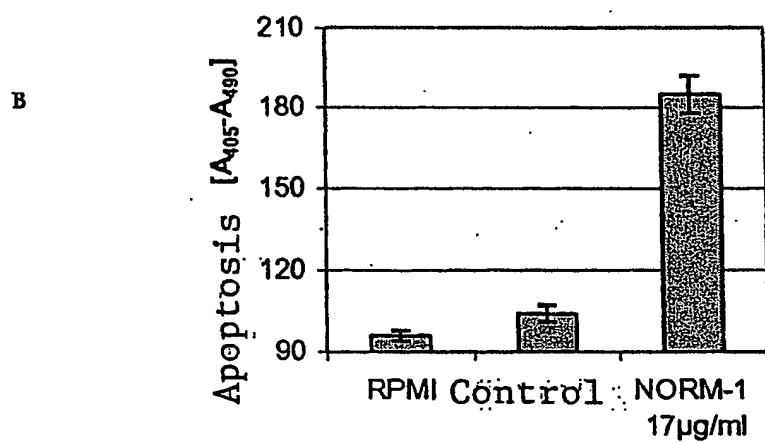
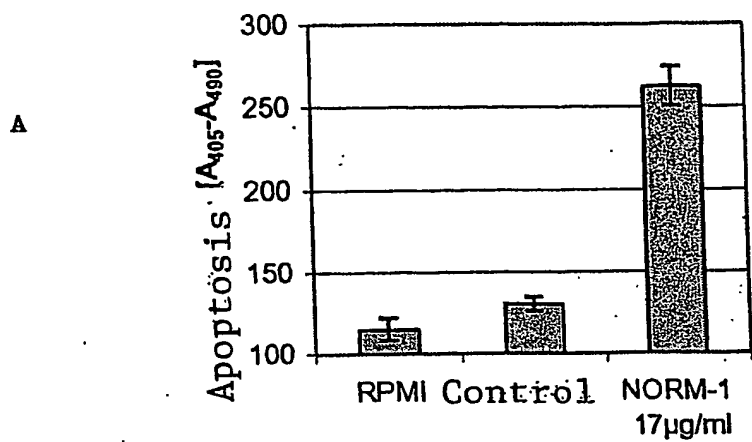


Fig. 5

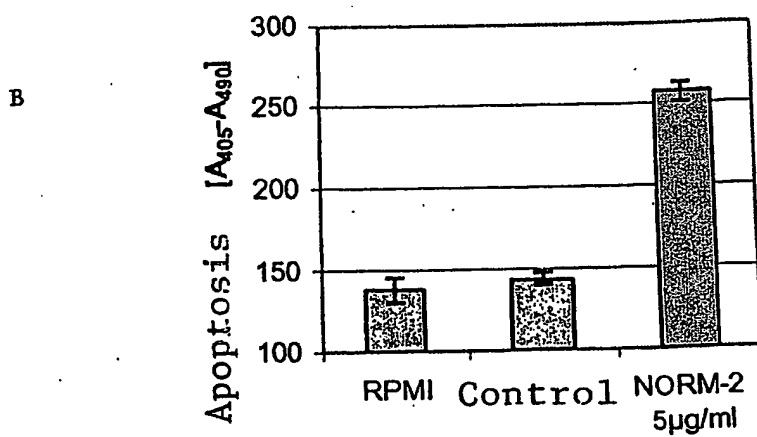
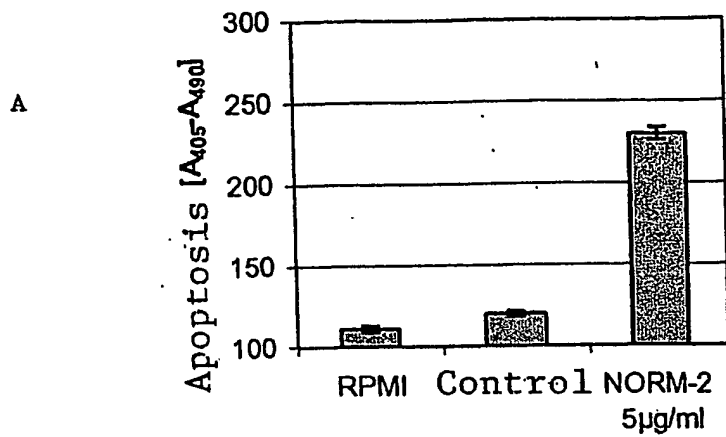


Fig. 6

NORM-1 (VH)

[illegible]

Fig. 7

NORM-1 (VL)

| | |
|---|-----|
| TCC TAT GTG CTG ACT CAG CCA CCC TCG GTG TCA GTG TCC CCA GGA CAA ACG GCC AGG ATC | 60 |
| Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln Thr Ala Arg Ile | 20 |
| 1 5 10 15 20 | |
| CDR1 | |
| 67 99 | |
| ACC TGC TCT GGA GAT GCA TTG CCA AAA AAA TAT GCT TAT TGG TAC CAG CAG AAG TCA GGC | 120 |
| Thr Cys Ser Gly Asp Ala Leu Pro Lys Lys Tyr Ala Tyr Trp Tyr Gln Gln Lys Ser Gly | 40 |
| 25 30 35 40 | |
| CDR2 | |
| 145 165 | |
| CAG GCC CCT GTG CTG ATC TAT GAG GAC AGC AAA CGA CCC TCC GGG ATC CCT GAG AGA | 180 |
| Gln Ala Pro Val Leu Val Ile Tyr Glu Asp Ser Lys Arg Pro Ser Gly Ile Pro Glu Arg | 60 |
| 45 50 55 60 | |
| CDR3 | |
| 262 297 | |
| GAT GAA GCT GAC TAC TAC TGT TAC TCA ACA GAC AGC AGT GGT AAT CAT AGC TAT GTG TTC | 300 |
| Asp Glu Ala Asp Tyr Tyr Cys Tyr Ser Thr Asp Ser Ser Gly Asn His Ser Tyr Val Phe | 100 |
| 85 90 95 100 | |

J-Region

Fig. 8

NORM-2 (VH)

| | |
|---|-----|
| GAG GTG CAG CTG GTG GAG TCT GGG GGA GGC CTG GTC AAG CCT GGG GGG TCC CTG AGA CTC | 60 |
| Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Lys Pro Gly Gly Ser Leu Arg Leu | 20 |
| 1 5 10 15 | |
| CDR1 | |
| TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT AGC TAT AGC ATG AAC TGG GTC CGC CAG GCT | 120 |
| Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ser Met Asn Trp Val Arg Gln Ala | 40 |
| 25 30 35 | |
| CDR2 | |
| CCA GGG AAG GGG CTG GAG TGG GTC TCA TCC ATT AGT AGT AGT AGT TAC ATA TAC TAC | 180 |
| Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Ser Ser Ser Tyr Ile Tyr Tyr | 60 |
| 45 50 55 | |
| GCA GAC TCA GTG AAG GGC CGA TTC ACC ATC TCC AGA GAC AAC GCC AAG AAC TCA CTG TAT | 240 |
| Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr | 80 |
| 65 70 75 | |
| D-Region | |
| CTG CAA ATG AAC AGC CTG AGA GCC GAG GAC ACG GCT GTG TAT TAC TGT GCG AGA CAT GGG | 300 |
| Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg His Gly | 100 |
| 85 90 95 | |
| CDR3 | |
| J-Region | |
| AAC TAC TAC TAC TAC ATG GAC GTC (SEQ. ID. NO: 6) | 324 |
| Asn Tyr Tyr Tyr Met Asp Val (SEQ. ID. NO: 5) | 105 |

Fig. 9

NORM-2 (VL)

CAG TCT GTG TTG ACG CAG CCG CCC TCA GTG TCT GGG GCC CCA GGG CAG AGG GTC ACC ATC 60
 Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile 20
 1 5 10 15 20

CDR1 108
 TCC TGC ACT GGG AGC AGC TCC AAC ATC GGG GCA GGT TAT GAT GTA CAC TGG TAC CAG CAG 120
 Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val His Trp Tyr Gln Gln 40
 25 30 35 40

CDR2 174
 CTT CCA GGA ACA GCC CCC AAA CTC CTC ATC TAT GGT AAC AGC AAT CGG CCC TCA GGG GTC 180
 Leu Pro Gly Thr Ala Pro Lys Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val 60
 45 50 55 60

CCT GAC CGG TTC TCT GGC TCC AAG TCT GGC ACC TCA GCC TCC CTG GCC ATC ACT GGG CTC 240
 Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu 80
 65 70 75 80

J-Region
 CDR3
 CAG GCT GAG GAT GAG GCT GAT TAT TAC TGC CAG TCC TAT GAC AGC AGC CTG AGT GCC TTG 300
 Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser Leu Ser Ala Leu 100
 85 90 95 100

303
 GTA TTC (SEQ. ID. NO: 8)
 Val Phe (SEQ. ID. NO: 7)

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